nf-core/ hackathon

October
2022

You

289

People registered

You

51

In person

238

Online

Groups

Documentation

Pipelines

Subworkflows

Modules

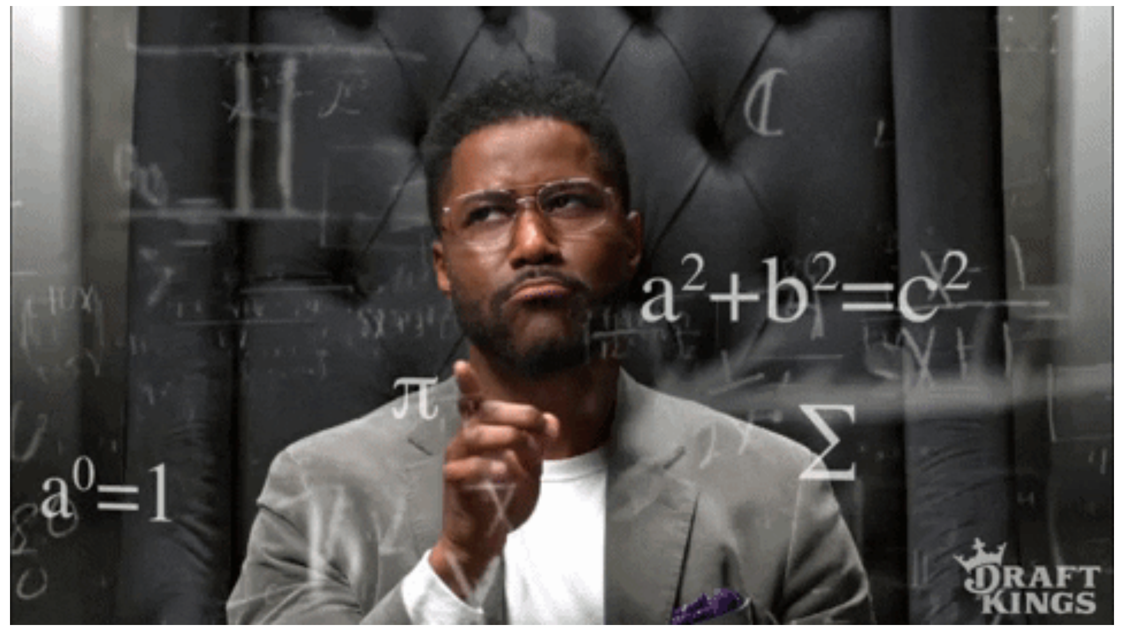
Infrastructure

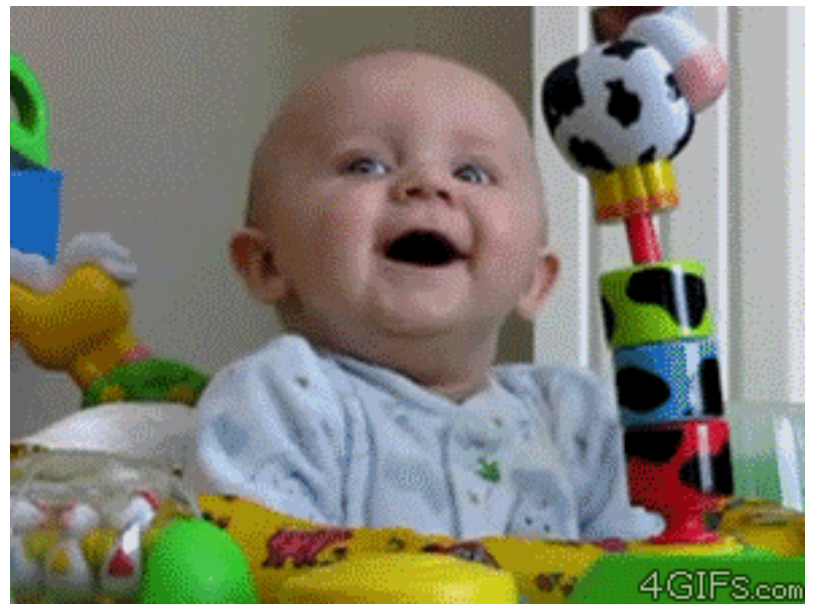
Documentation

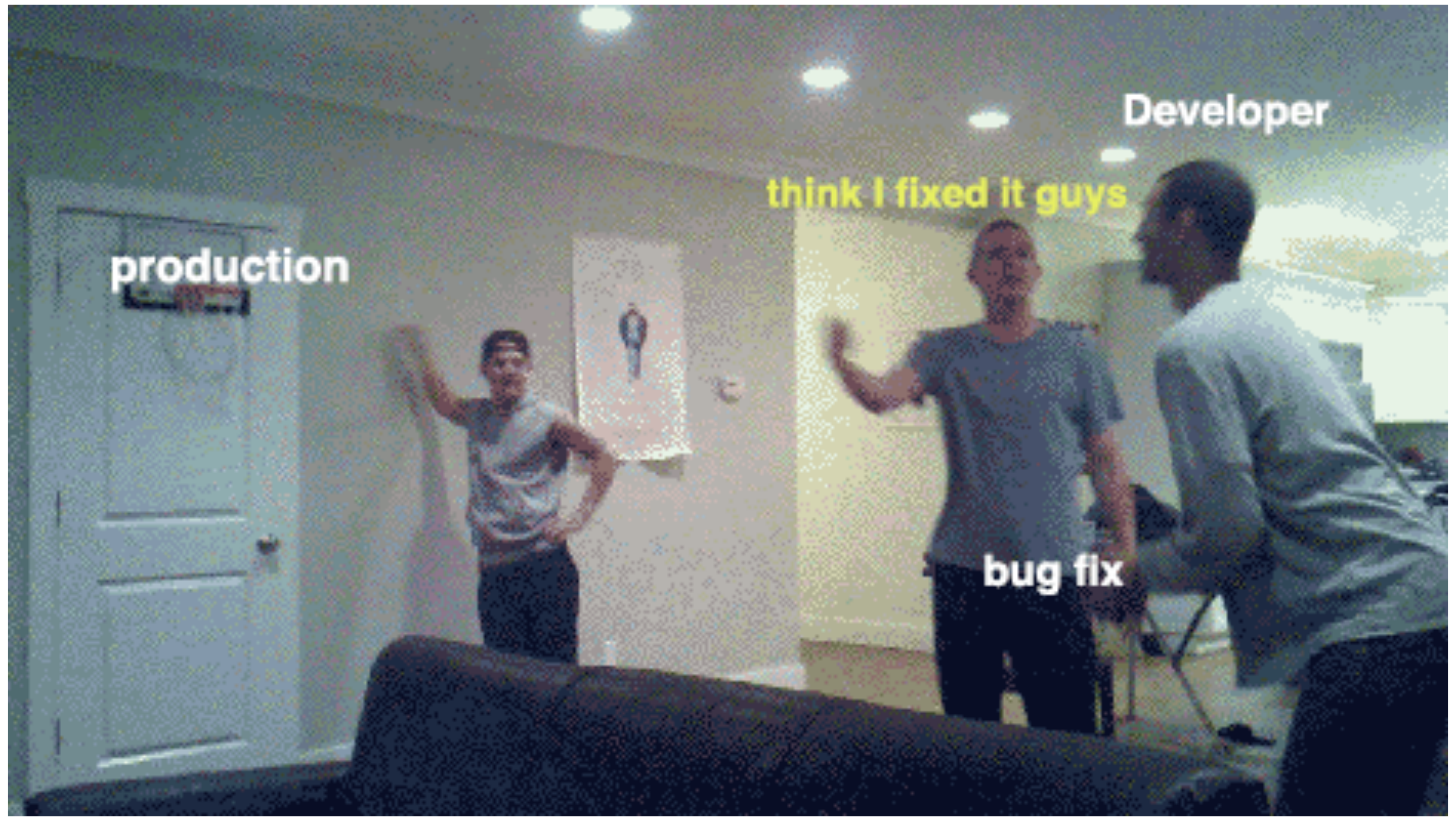
- 50+ PRs with 48 merged and 3 ready-for-review 👏
- Highlights
  - Inter-group cooperation
  - Good online and offline engagement
  - Increased confidence in contributions

Reviewing Buddy List

Person A	Person B
Maxime	Rike
James	Rike
Alex	Rob
Luis	Hanka
Alison	Oliver
Aaron	Luis

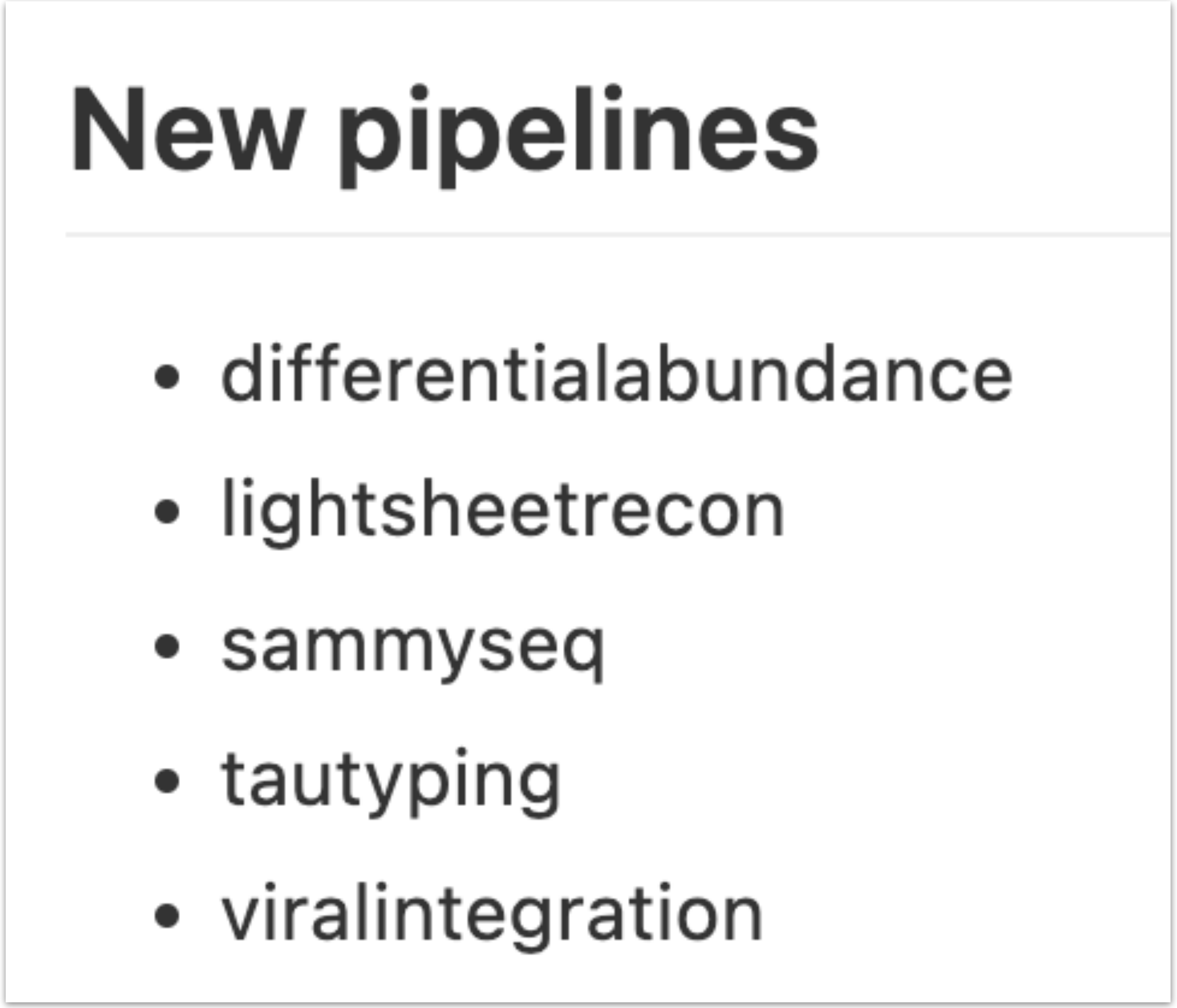






Pipelines

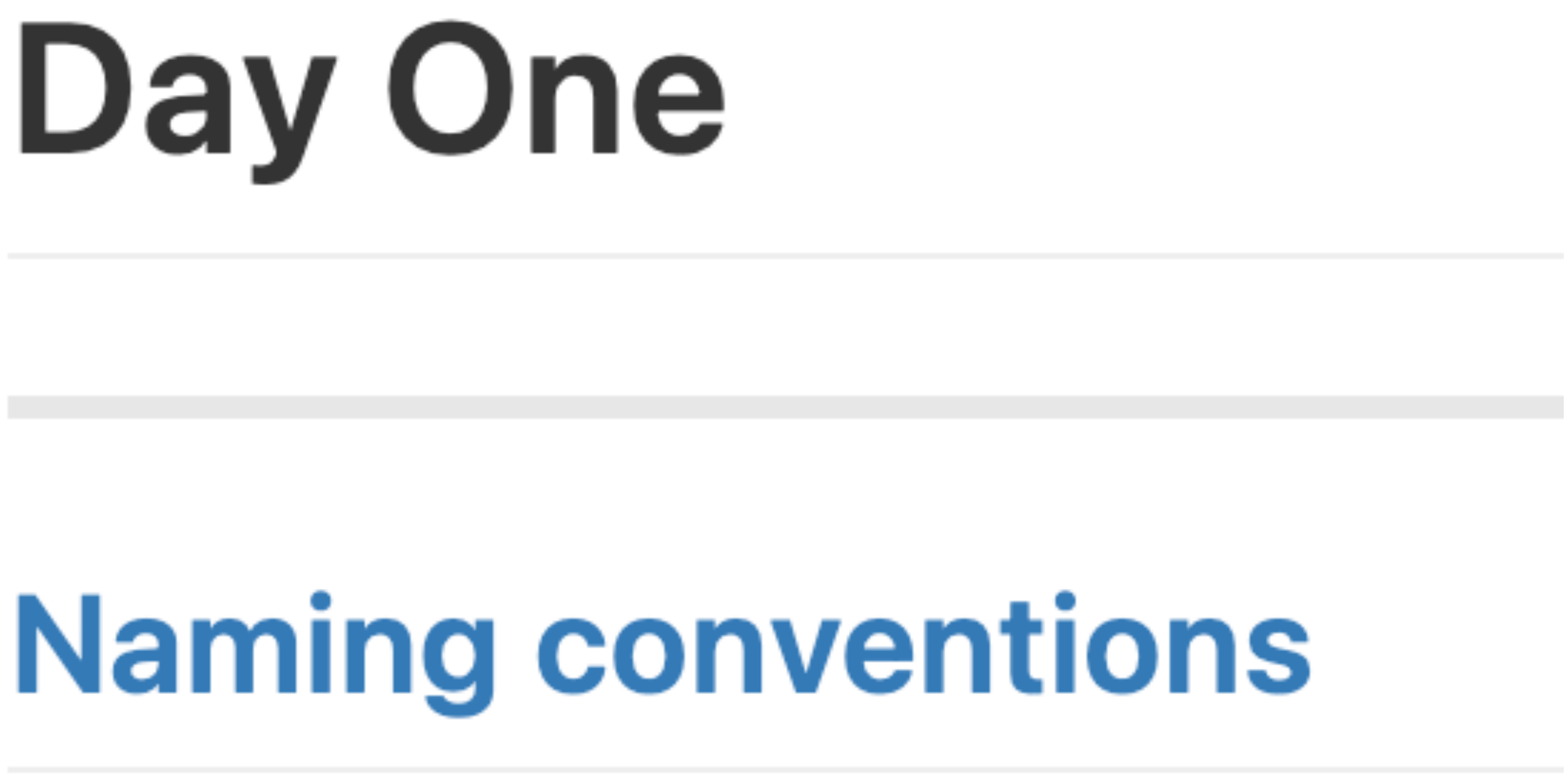
- eager
- sarek
- liverctanalysis
- funcscan
- airrflow
- smrnaseq
- tautyping
- hgtseq
- proteinfold
- taxprofiler
- differentialabundance
- viralintegration
- nascent



New pipelines

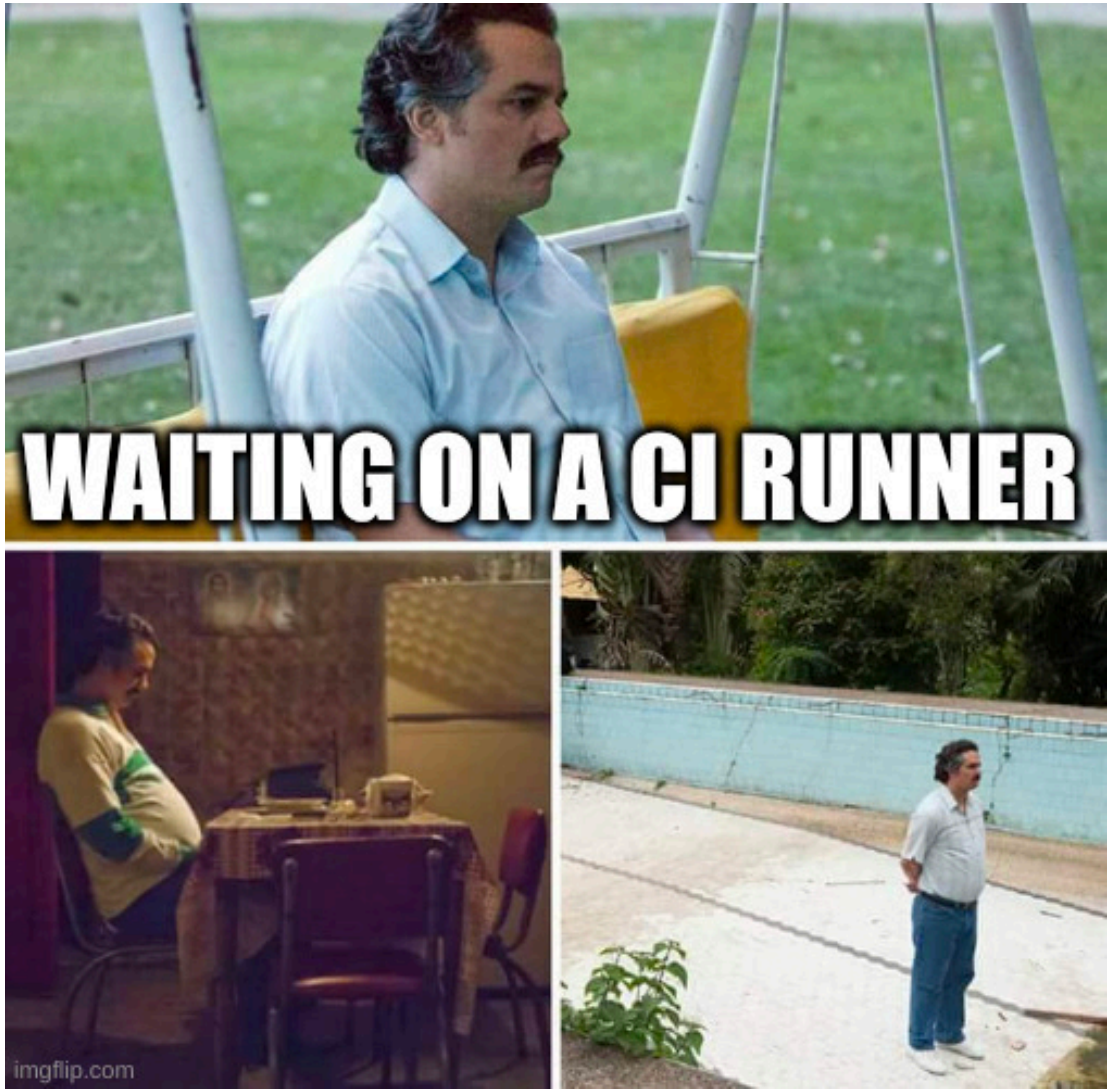
- differentialabundance
- lightsheetrecon
- sammyseq
- tautyping
- viralintegration

Subworkflows

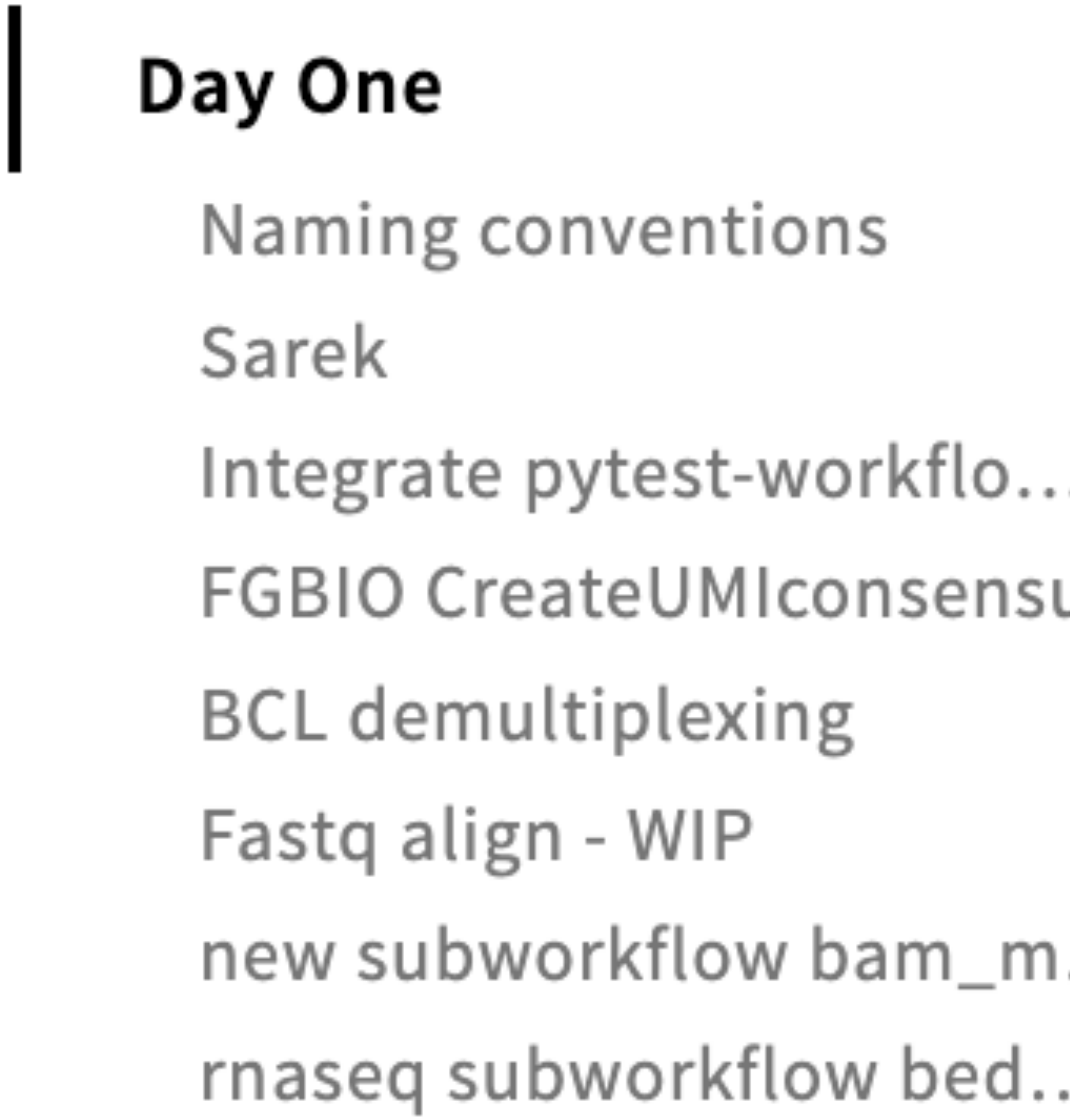


Day One

Naming conventions

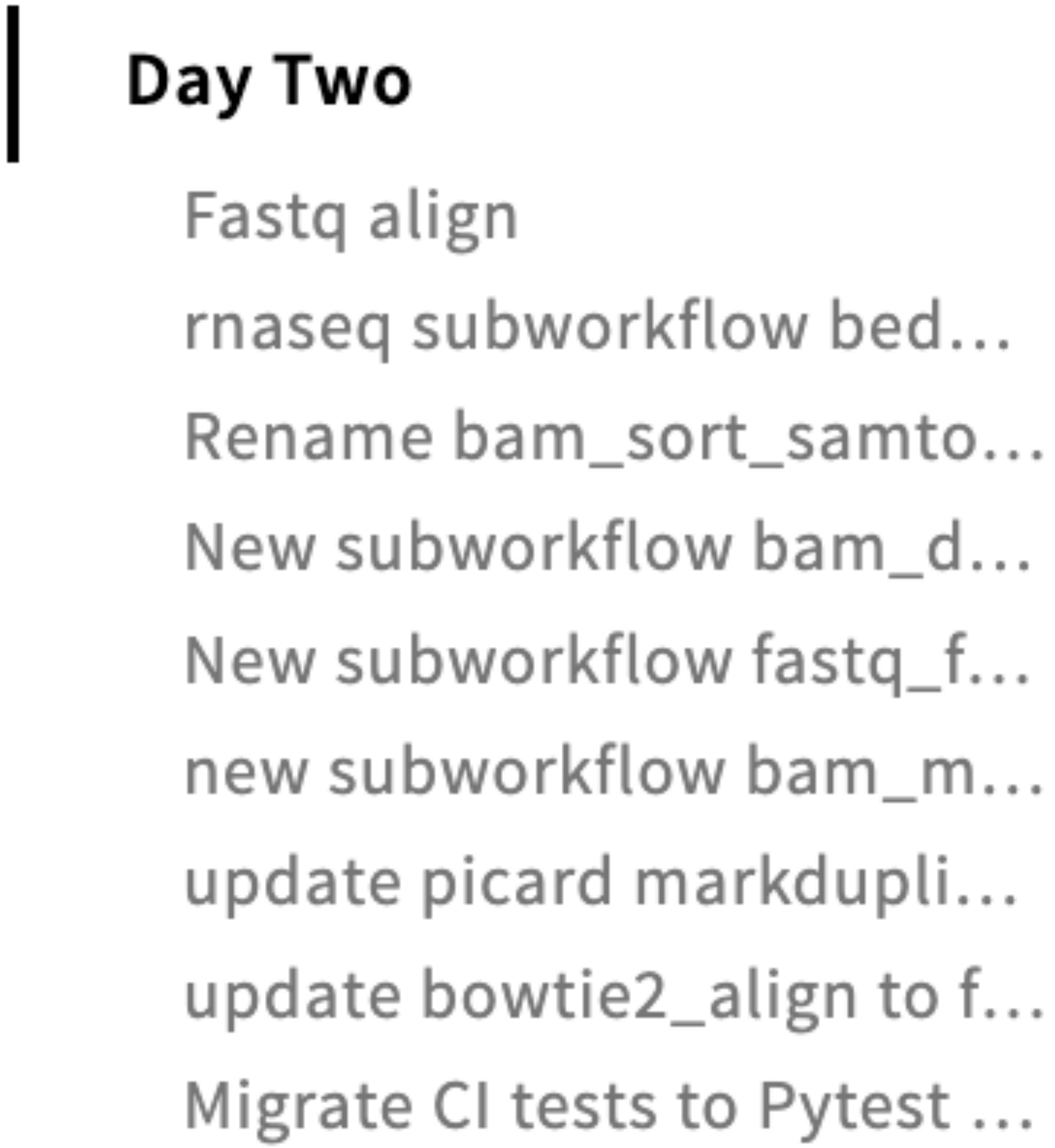


Subworkflows



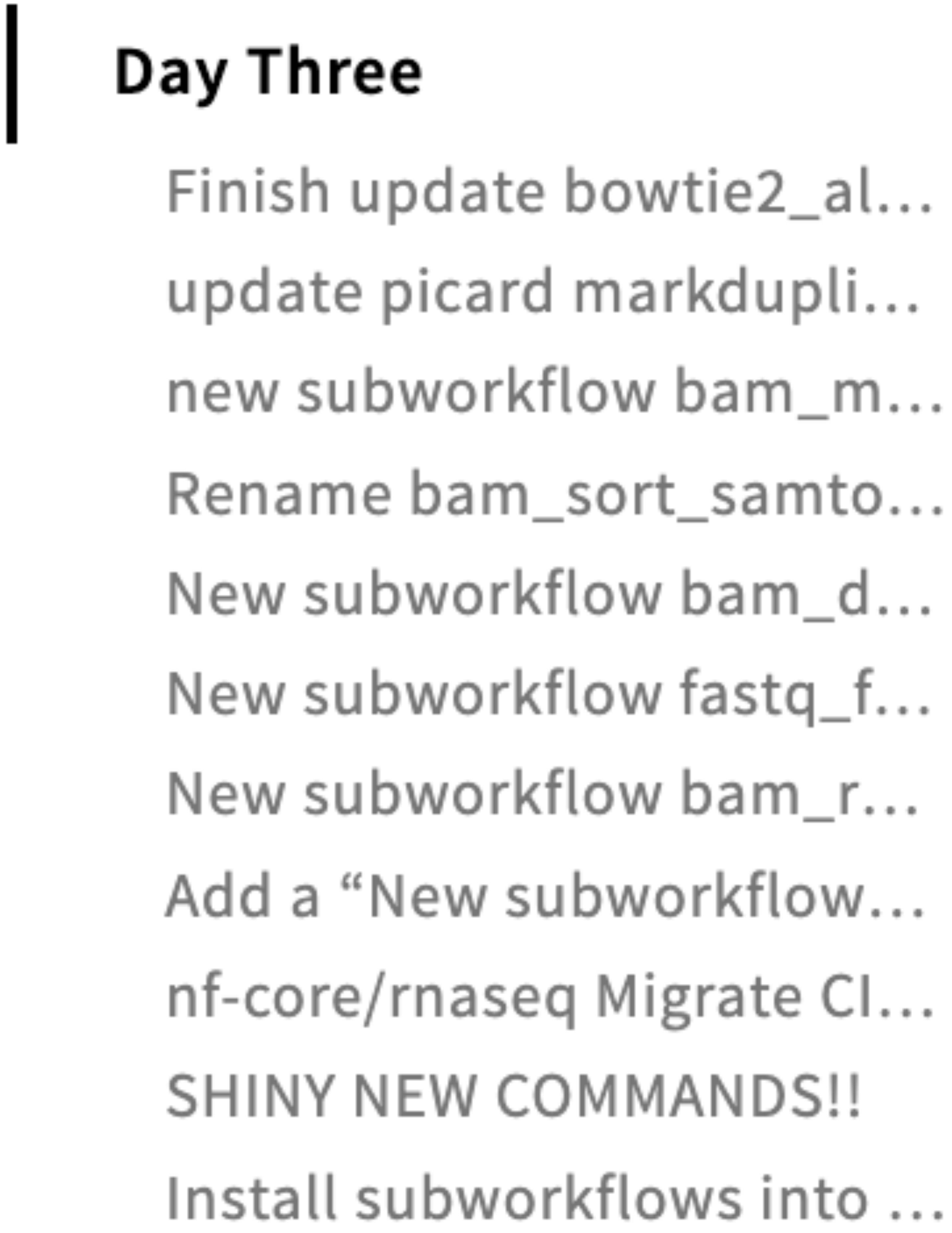
Day One

Naming conventions
Sarek
Integrate pytest-workflo..
FGBIO CreateUMIconsensu
BCL demultiplexing
Fastq align - WIP
new subworkflow bam_m.
rnaseq subworkflow bed..



Day Two

Fastq align
rnaseq subworkflow bed…
Rename bam_sort_samto…
New subworkflow bam_d…
New subworkflow fastq_f…
new subworkflow bam_m…
update picard markdupli…
update bowtie2_align to f…
Migrate CI tests to Pytest …

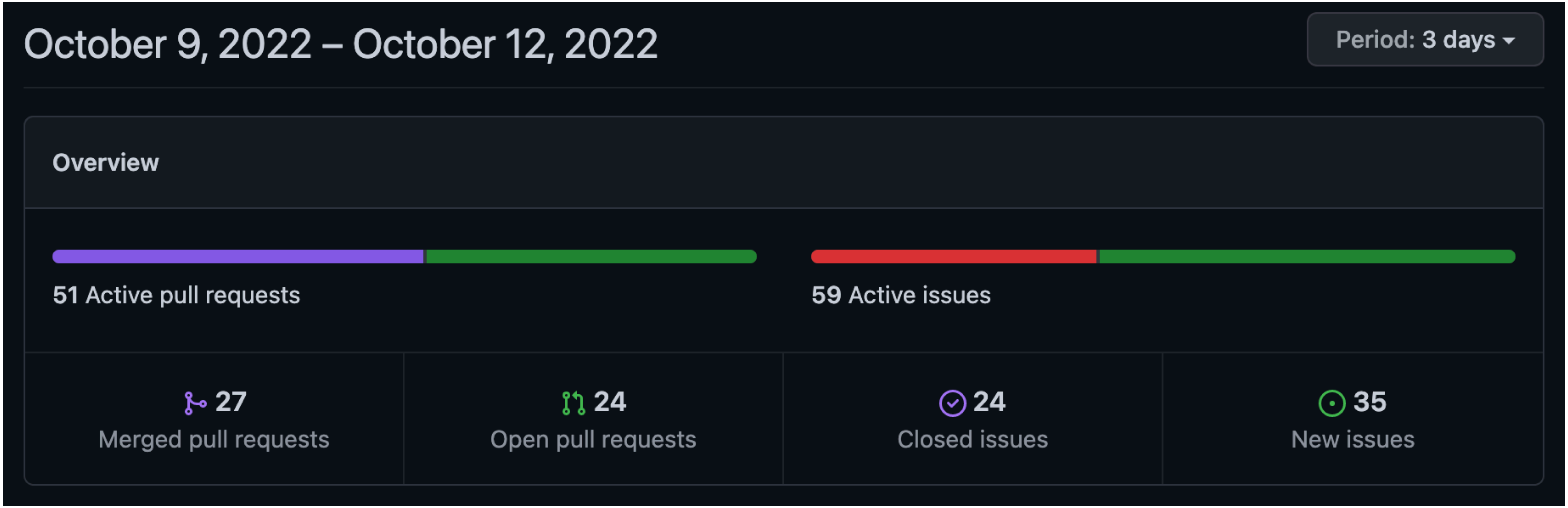


Day Three

Finish update bowtie2_al…
update picard markdupli…
new subworkflow bam_m…
Rename bam_sort_samto…
New subworkflow bam_d…
New subworkflow fastq_f…
New subworkflow bam_r…
Add a “New subworkflow…
nf-core/rnaseq Migrate CI…
SHINY NEW COMMANDS!!
Install subworkflows into …

Subworkflows

Modules



October 9, 2022 – October 12, 2022

Overview

51 Active pull requests

59 Active issues

27 Merged pull requests

24 Open pull requests

24 Closed issues

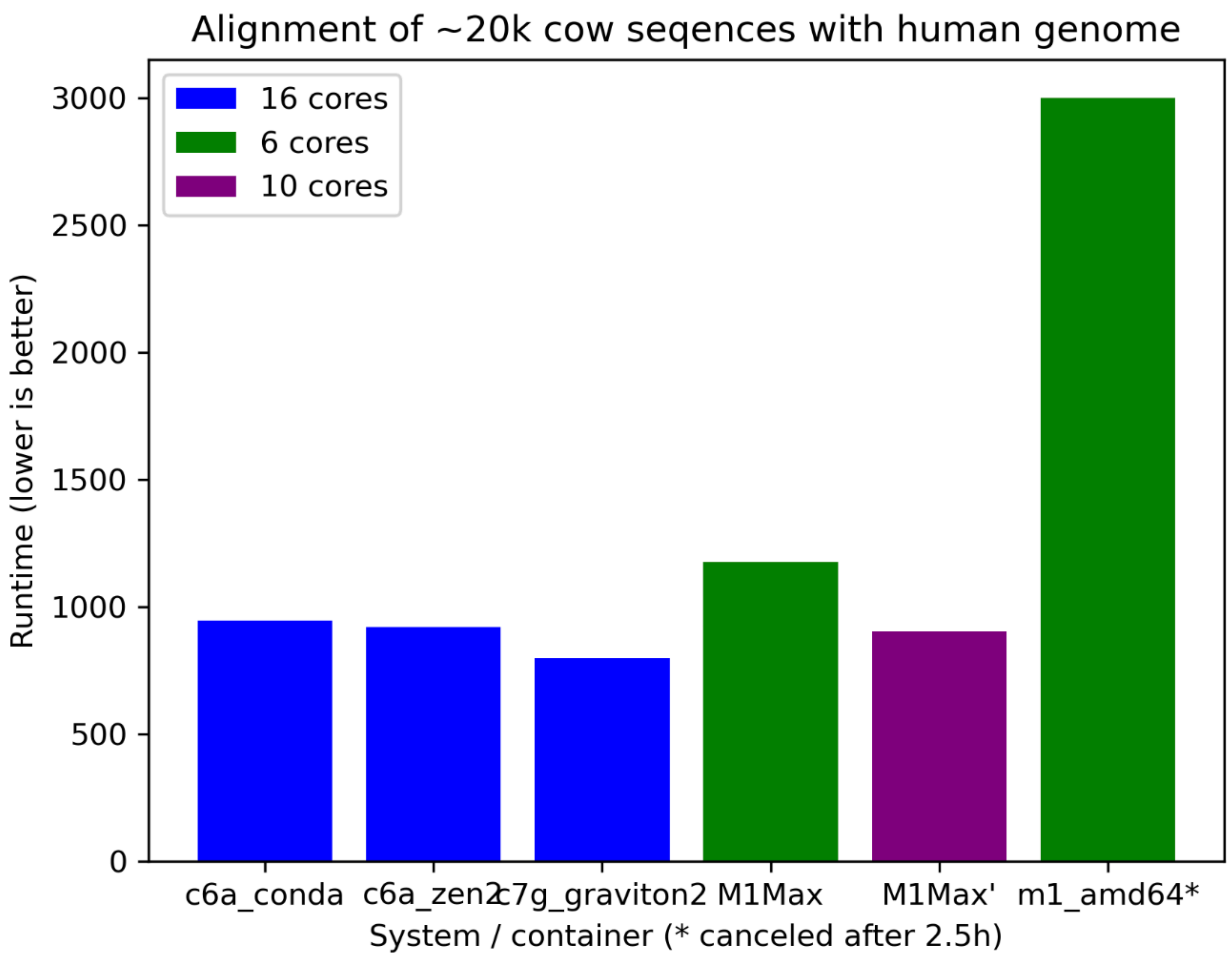
35 New issues

Modules

Running docker on M1 chips

M1 `--platform=linux/amd64` uses VM which degrades performance (@ChristianKniep @snafees)

- most likely depending on the tool (simple python scripts might work just fine)
- of course: **running slow** is always better than **not running at all**



General updates

- Alison reviewing PRs and triggering discussion of **task.ext.args**. Params should not be passed as value channels to modules unless they are needed in the script section (e.g. if/else statements.)
- Jennifer updated the documentation on that in the modules guidelines

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New modules

- Anan and Louisa continued on the **AMPcombi** module, writing tests now.
- Alan added the test RNA BAM files and has a working **ABRA2 module** locally #2186. Pull request (#2288)[https://github.com/nf-core/modules/pull/2288] created.

New modules

- Sreeram had to continue working on module **repeatscout** (creating subtools instead of one main tool).
- Ilja is working on the **repeatscout submodules**.
- Saba and Gisela worked on the **presto/filterseq** module. Getting tests to pass on CI.
- Maulik was working on **fulcrumgenomics/fqgrep** #1941; the tool search for user-defined refernce and alternative sequence in the paired-end fastq file https://github.com/BioInf2305/fqgrep-in-progress

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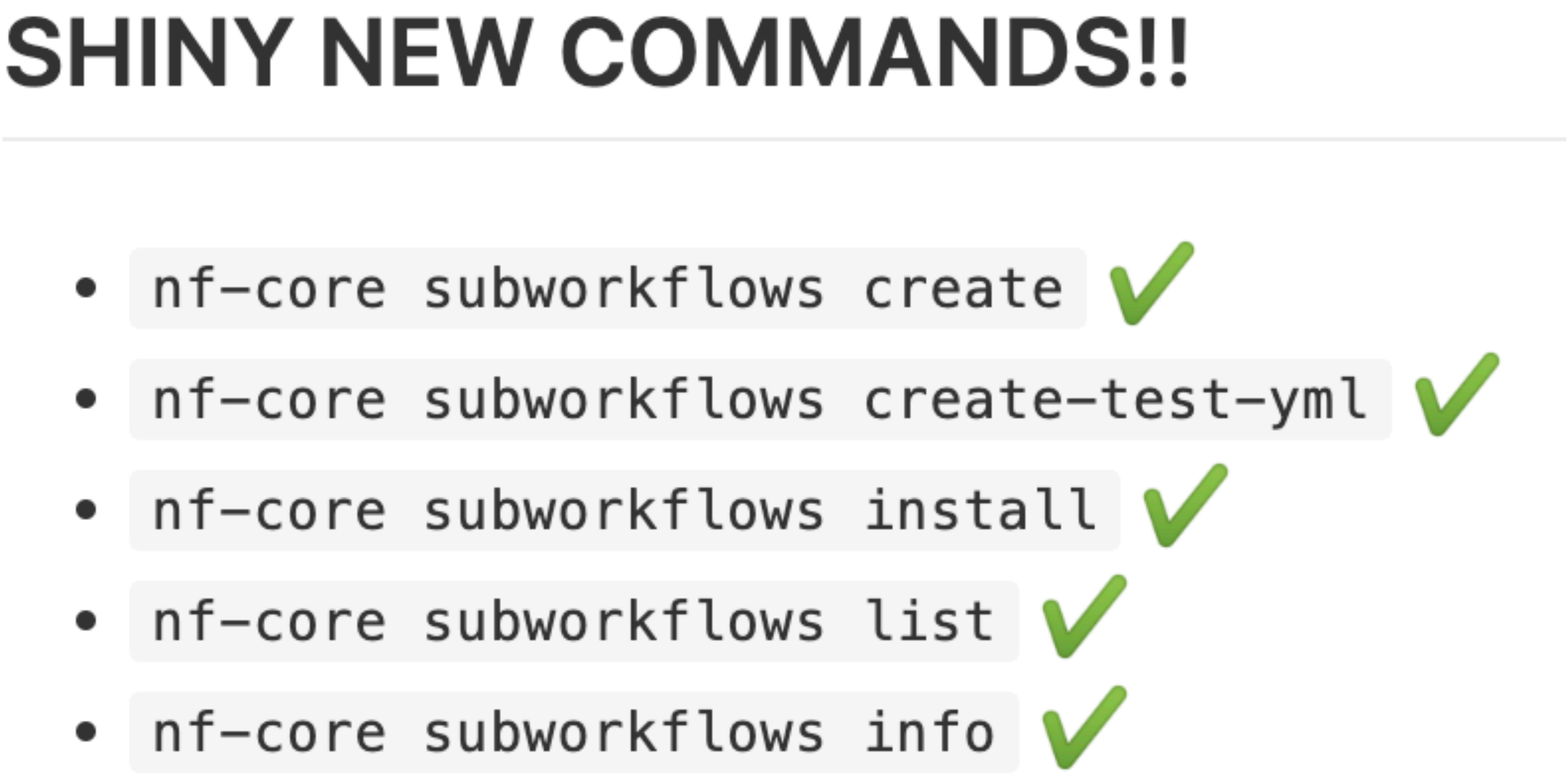
Module fixes

- Drop endedness check for **Fastqc** - https://github.com/nf-core/modules/issues/2278 & https://github.com/nf-core/modules/pull/2282
- Luca and Matthias updated **FastQC** and **Falco**. The **meta.single_end** is now ignored, the tools will just check for the number of files.
- Robert fixed **smoove** container on Biocontainers

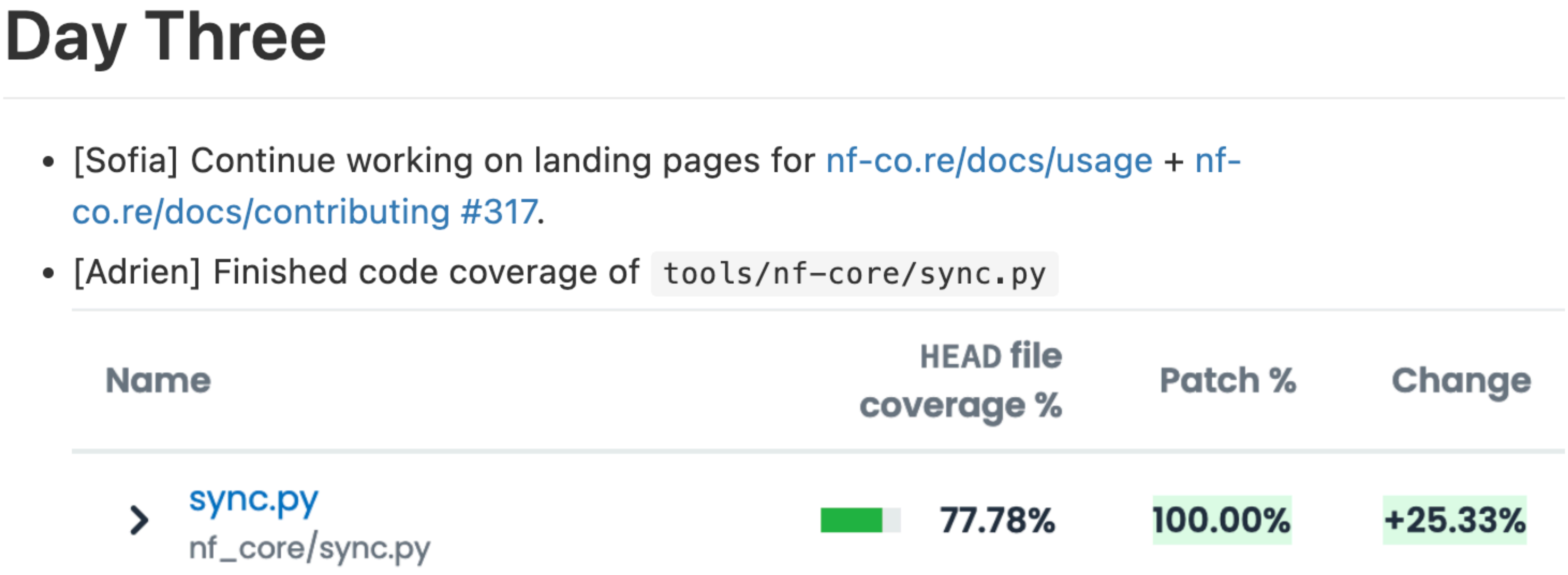
Infrastructure



SHINY NEW COMMANDS!!

- `nf-core subworkflows create` ✓
- `nf-core subworkflows create-test-yml` ✓
- `nf-core subworkflows install` ✓
- `nf-core subworkflows list` ✓
- `nf-core subworkflows info` ✓

Infrastructure



Day Three

- [Sofia] Continue working on landing pages for nf-co.re/docs/usage + nf-co.re/docs/contributing #317.
- [Adrien] Finished code coverage of `tools/nf-core/sync.py`

Name	HEAD file coverage %	Patch %	Change
sync.py nf_core/sync.py	77.78%	100.00%	+25.33%

nf-test 🚀

nf-prov 📐

Stats

Matthias Hörtenhuber

@mashehu

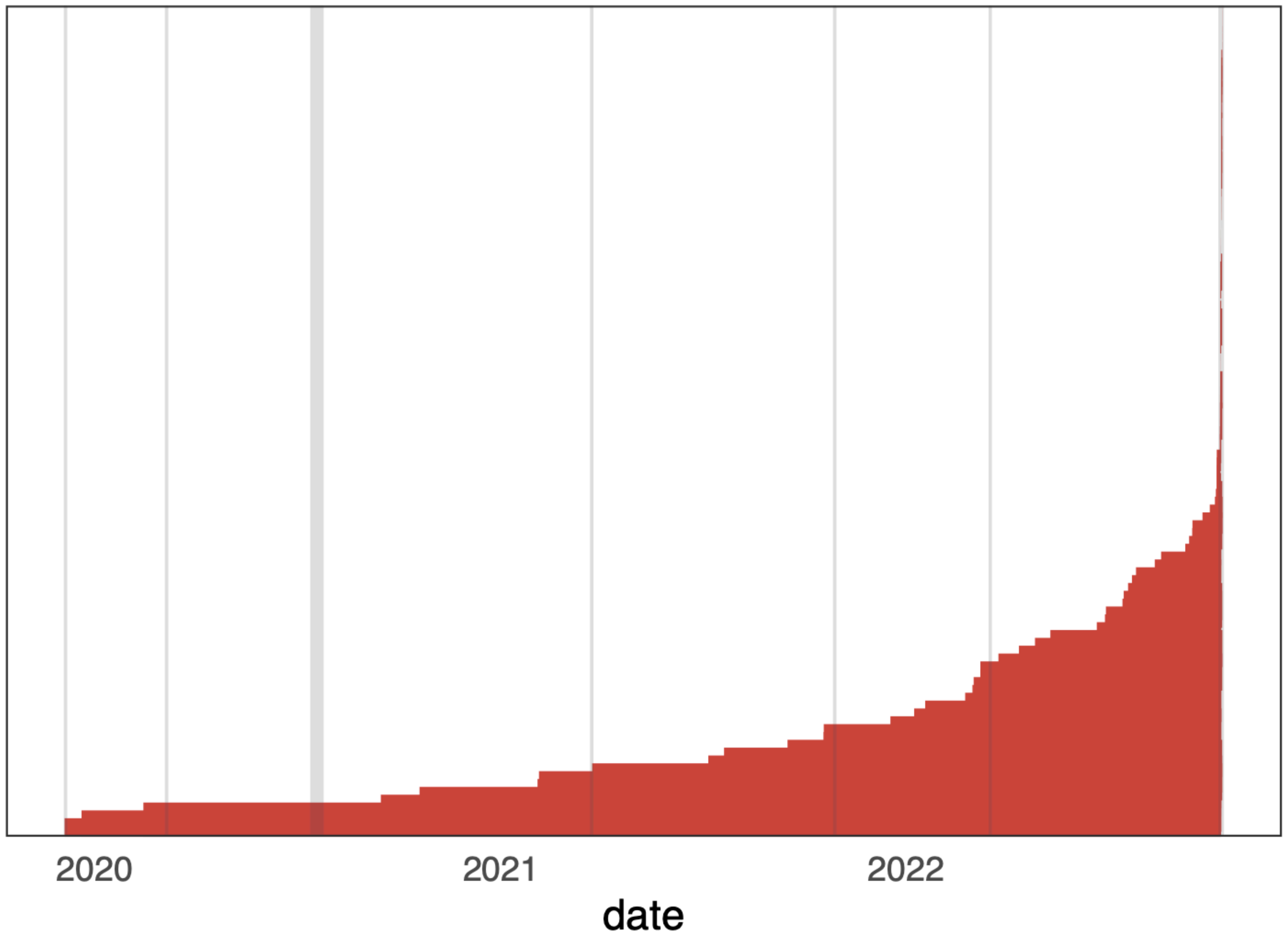
Stats

320	Open pull request
194	Merged pull request
298	Open issue
108	Closed issue

Stats

life span of issues closed

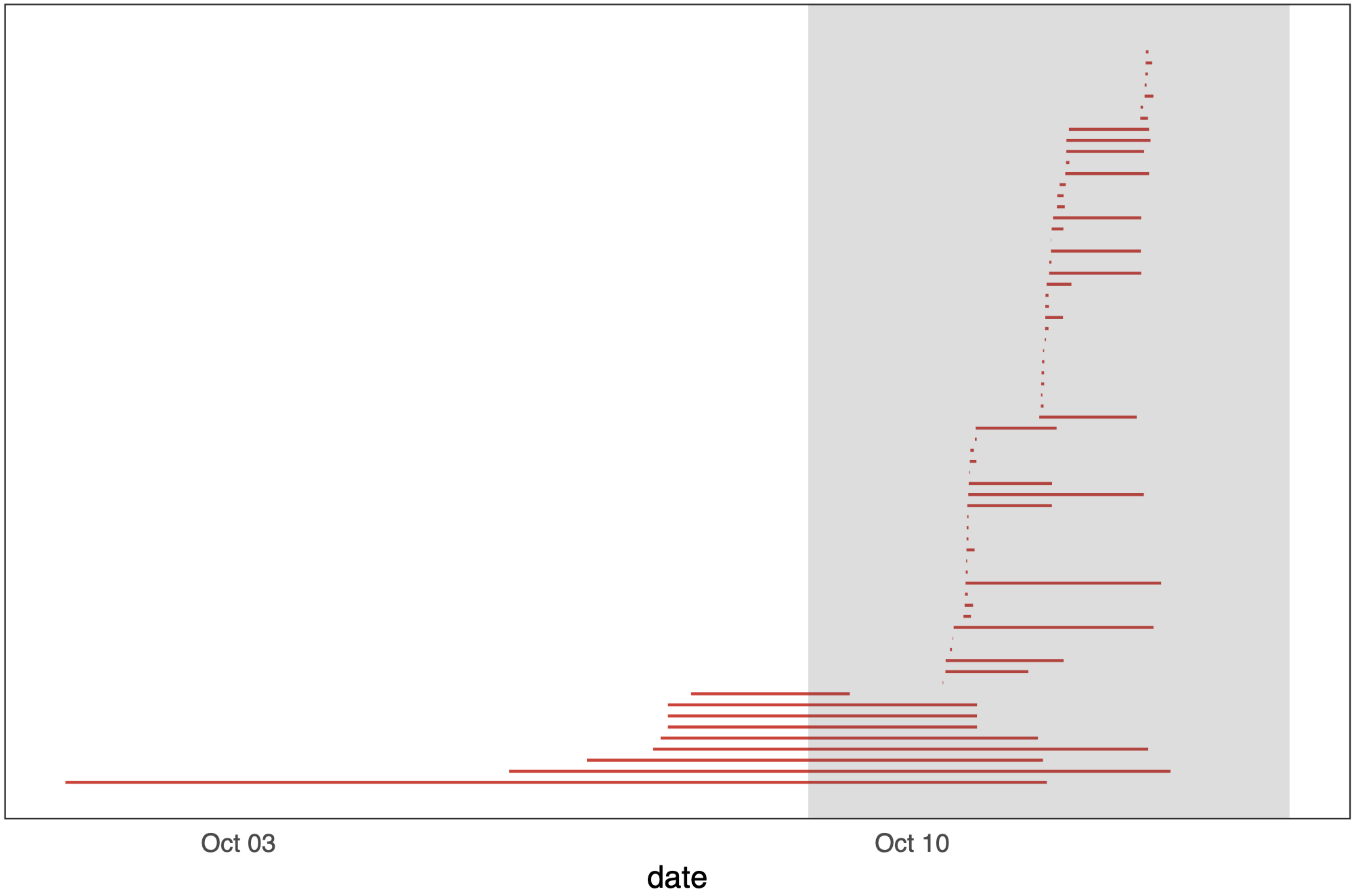
during the hackathon



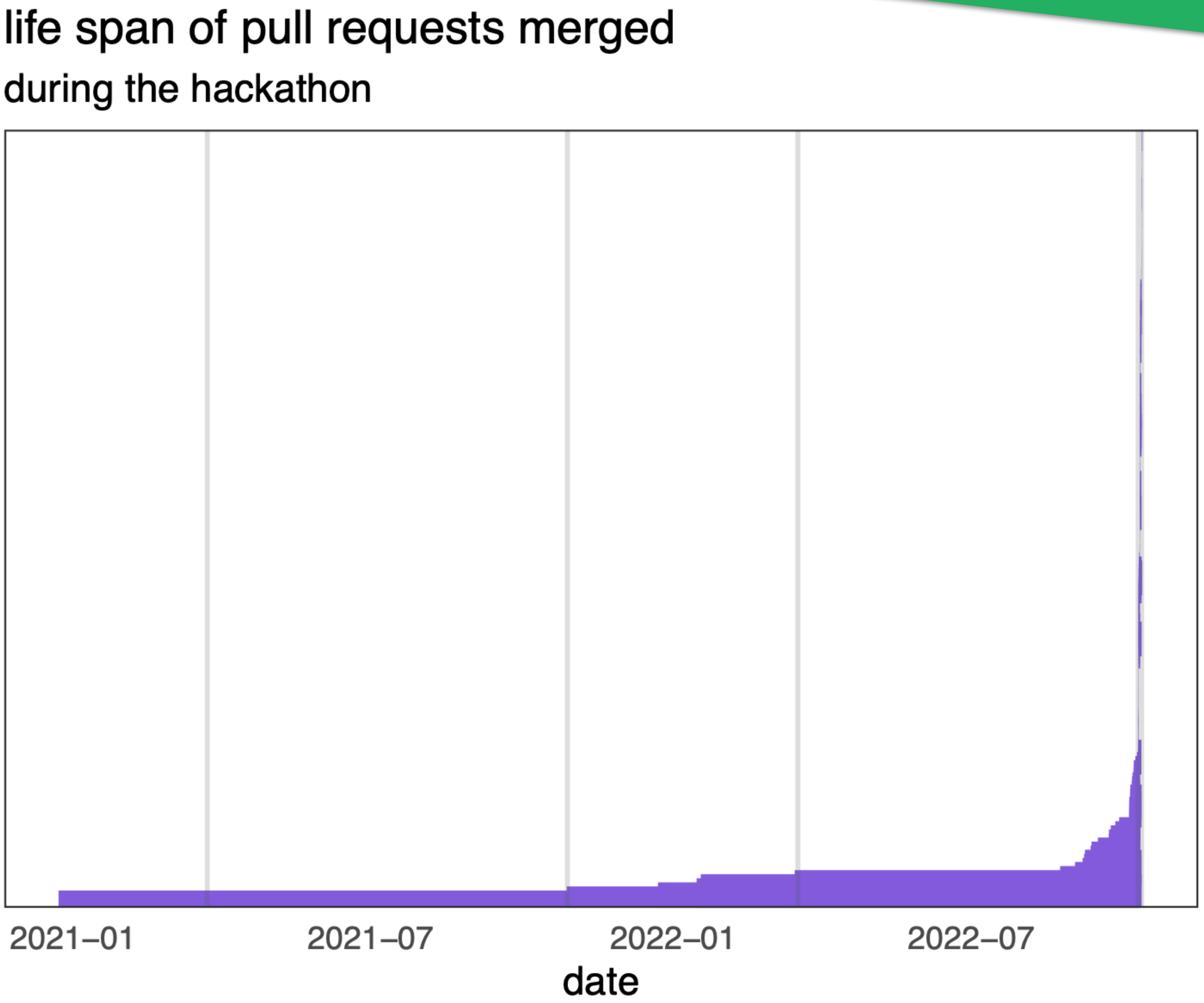
Stats

life span of issues closed

during the hackathon



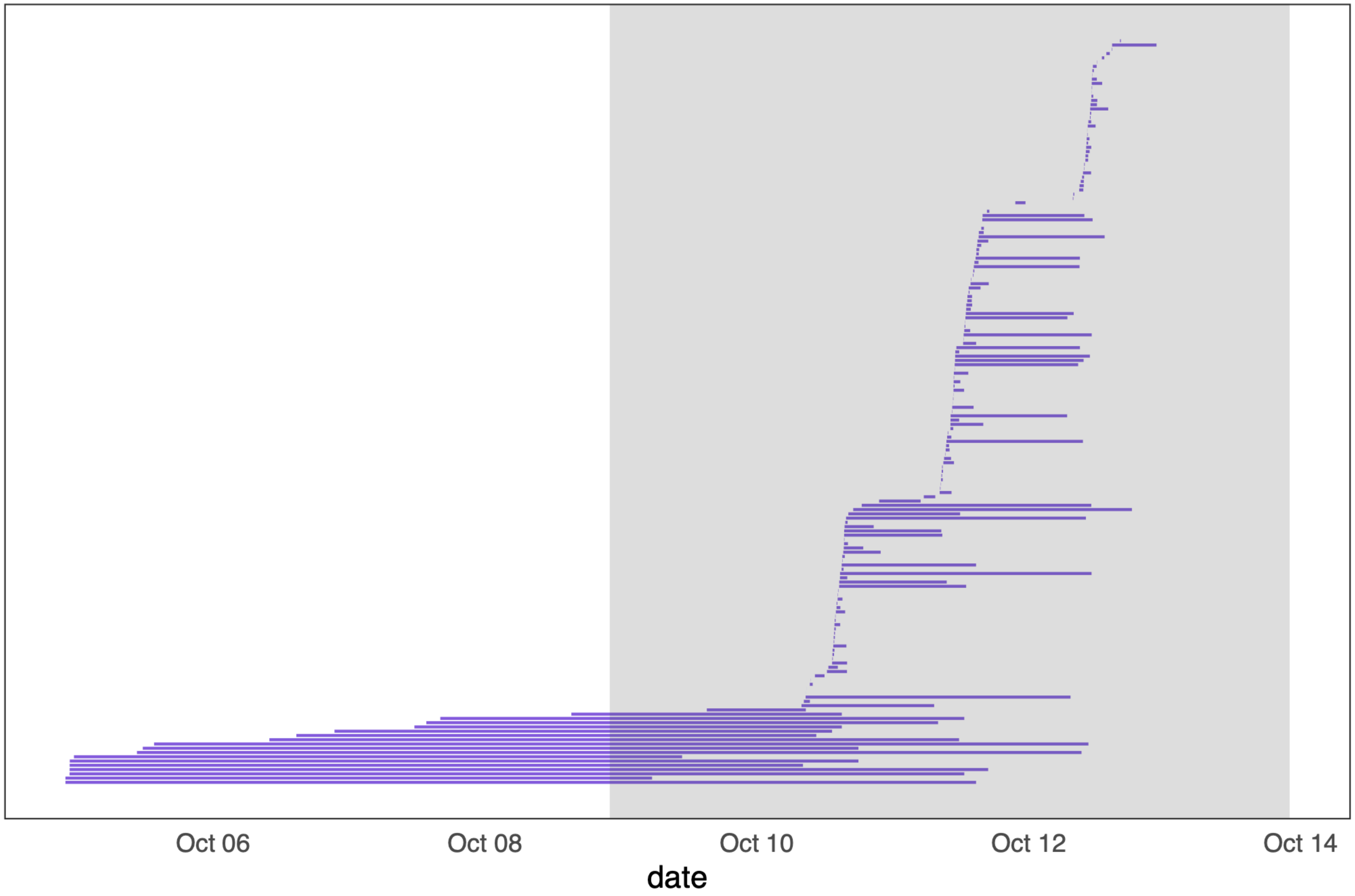
Stats


life span of pull requests merged
during the hackathon
2021–01
2021–07
2022–01
2022–07
date

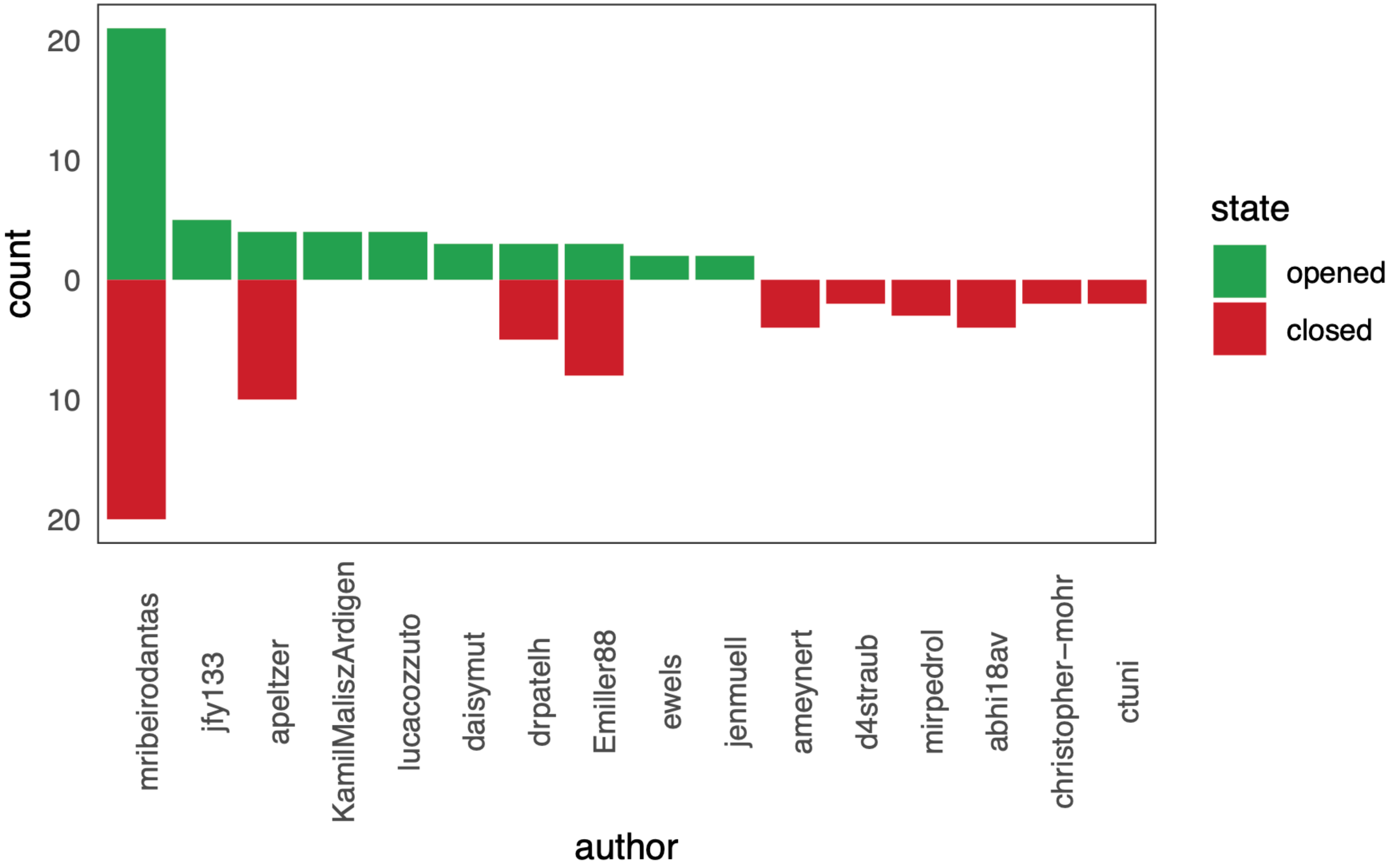
Stats

life span of pull requests merged

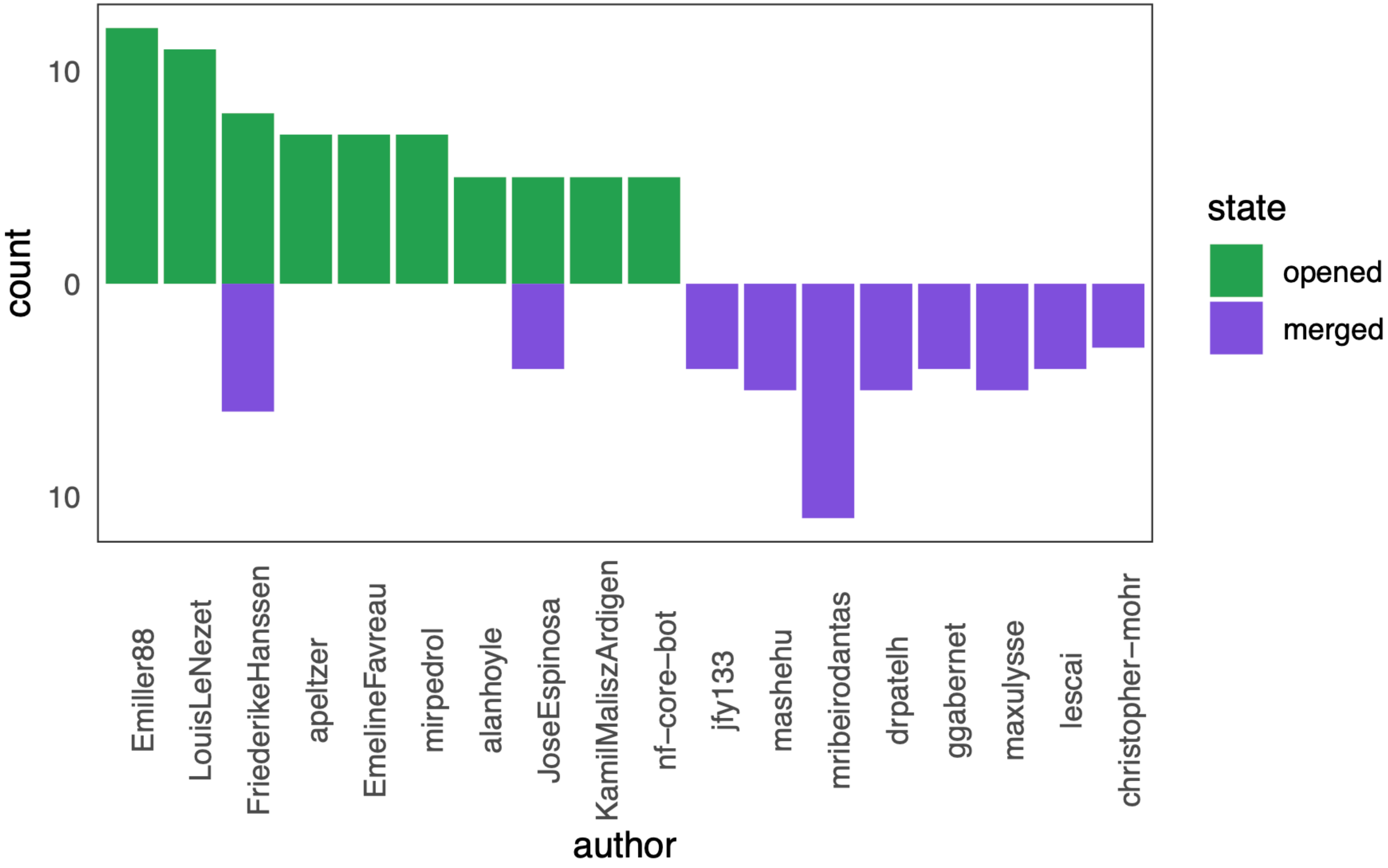
during the hackathon



Issue authors



PR authors



count
10
0
10
author
Emiller88
LouisLeNezet
FriederikeHanssen
apeltzer
EmelineFavreau
mirpedrol
alanhoyle
JoseEspinosa
KamilMaliszArdigen
nf–core–bot
jfy133
mashehu
mribeirodantas
drpatelh
ggabernet
maxulysse
lescai
christopher–mohr
state
opened
merged

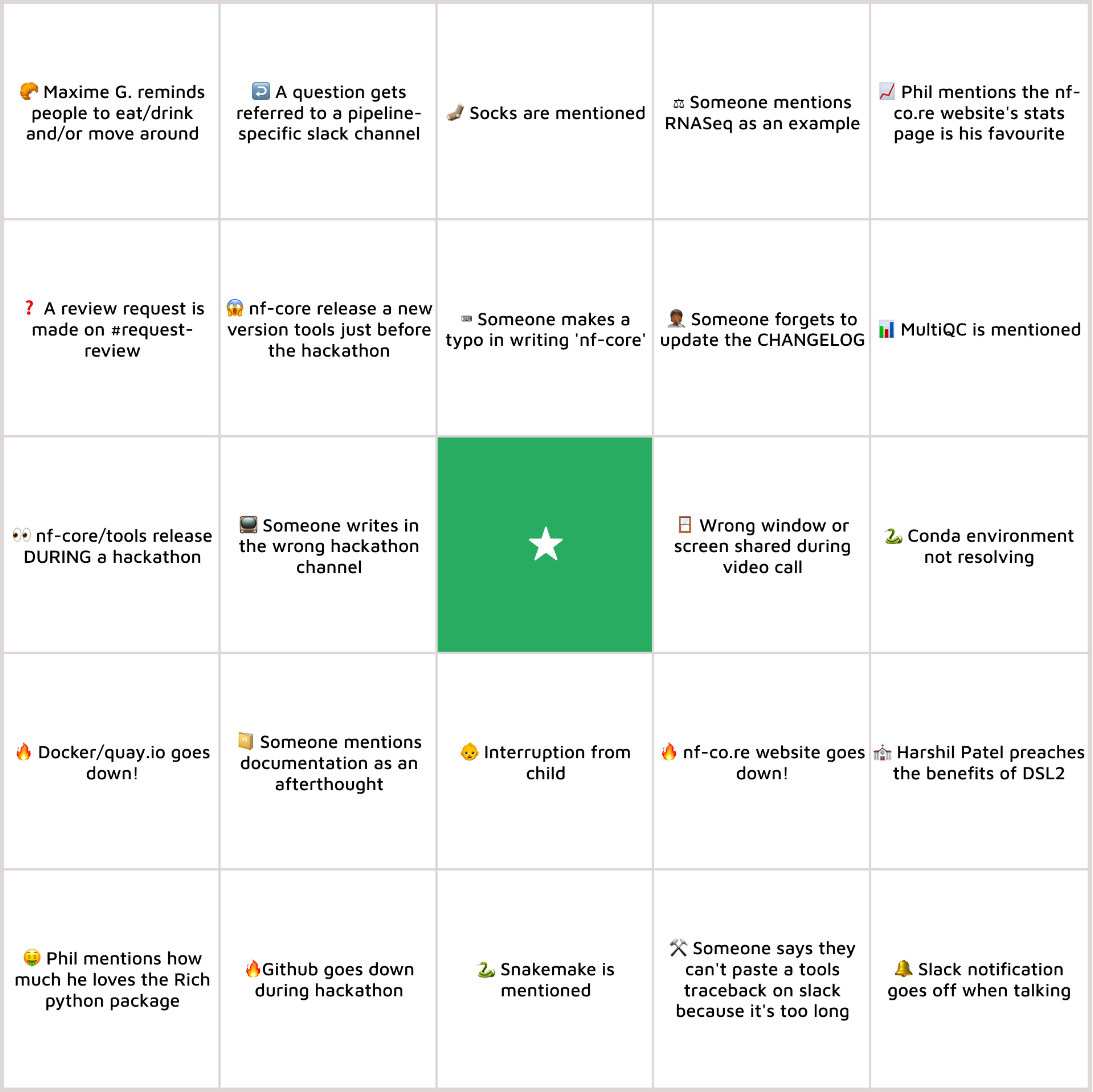
Social

Bingo

Find the socks

Kahoot Quiz (Wednesday)

Bingo



🥐 Maxime G. reminds people to eat/drink and/or move around	🔄 A question gets referred to a pipeline-specific slack channel	🧦 Socks are mentioned	⚖️ Someone mentions RNASeq as an example	📈 Phil mentions the nf-co.re website's stats page is his favourite
❓ A review request is made on #request-review	😱 nf-core release a new version tools just before the hackathon	⌨️ Someone makes a typo in writing 'nf-core'	🤦 Someone forgets to update the CHANGELOG	📊 MultiQC is mentioned
👀 nf-core/tools release DURING a hackathon	💻 Someone writes in the wrong hackathon channel	★	🪟 Wrong window or screen shared during video call	🐍 Conda environment not resolving
🔥 Docker/quay.io goes down!	📒 Someone mentions documentation as an afterthought	👶 Interruption from child	🔥 nf-co.re website goes down!	⛪ Harshil Patel preaches the benefits of DSL2
🤑 Phil mentions how much he loves the Rich python package	🔥Github goes down during hackathon	🐍 Snakemake is mentioned	⚒️ Someone says they can't paste a tools traceback on slack because it's too long	🔔 Slack notification goes off when talking

nf-core/bingo

Nicolas Vannieuwkerke 🏆

Laurence Kuhlburger

David Marron

Socks

:nf-core-socks:

:nf-core-umbrella:

:nf-core-apron:

Chan Zuckerberg Initiative

Essential Open Source Software for Science

Socks

@Victor Barrera (day 1: 14:51) 🏆

@Anandashankar Anil (day 1: 14:52)

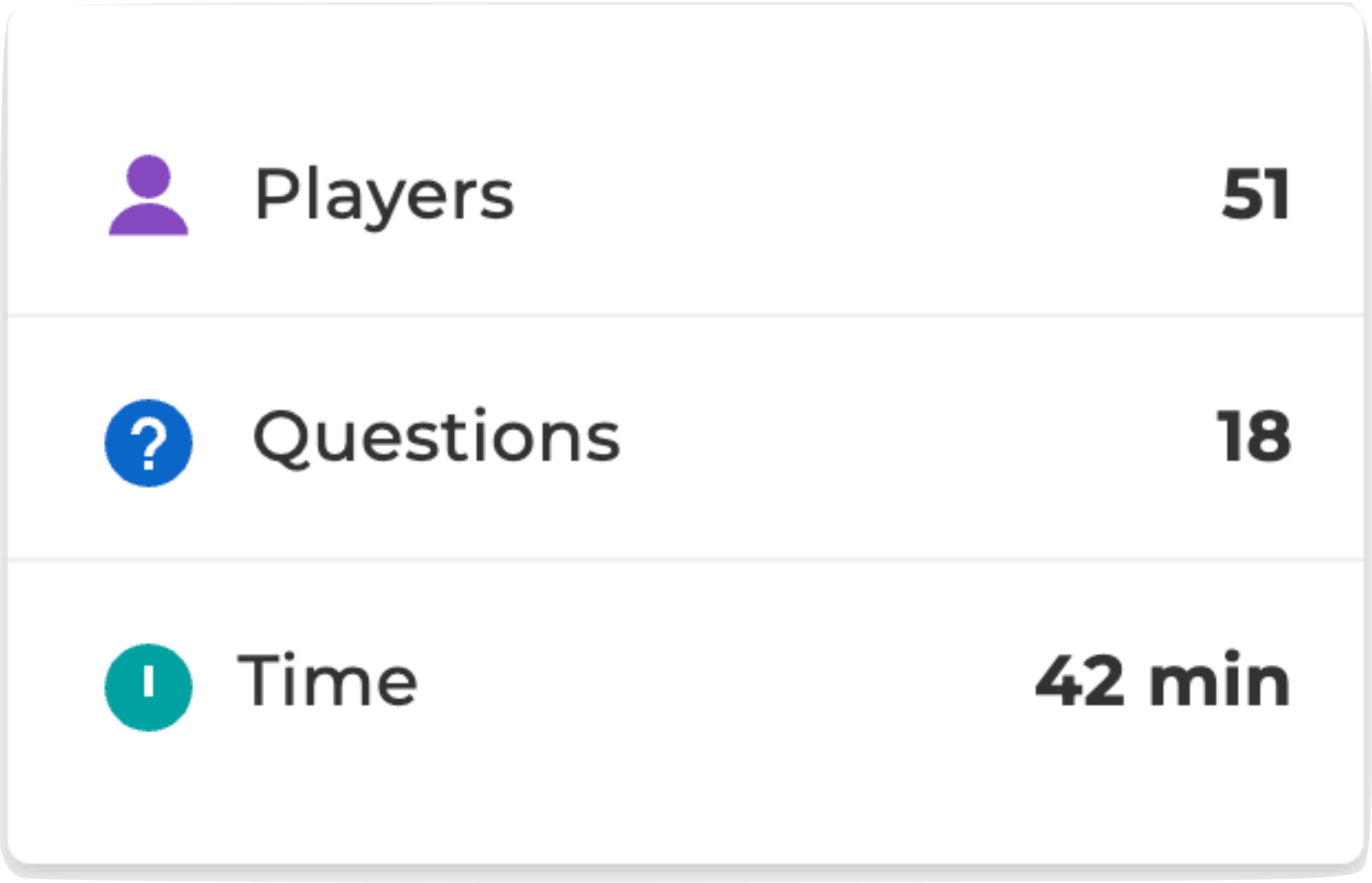
@Matthias Zepper (day 1: 15:14)

@Louis Le Nézet (day 1: 15:15)
@Louisa Perelo (day 1: 15:35)
@Pauline Auffret (day 1: 17:13)
@Nicolas Vannieuwkerke (day 2: 13:45)
@Susanne Jodoin (day 2: 13:46)
@Matthias De Smet (day 2: 13:57)
@Júlia Mir (day 2: 15:23)
@Solenne Correard (day 2: 15:49)
@Björn Langer (day 2: 18:28)

Kahoot


nextflow
The leading workflow orchestrator for computational, data-intensive pipelines
Kahoot!

Kahoot



Players	51
Questions	18
Time	42 min

Need help (12)

Kahoot

12%

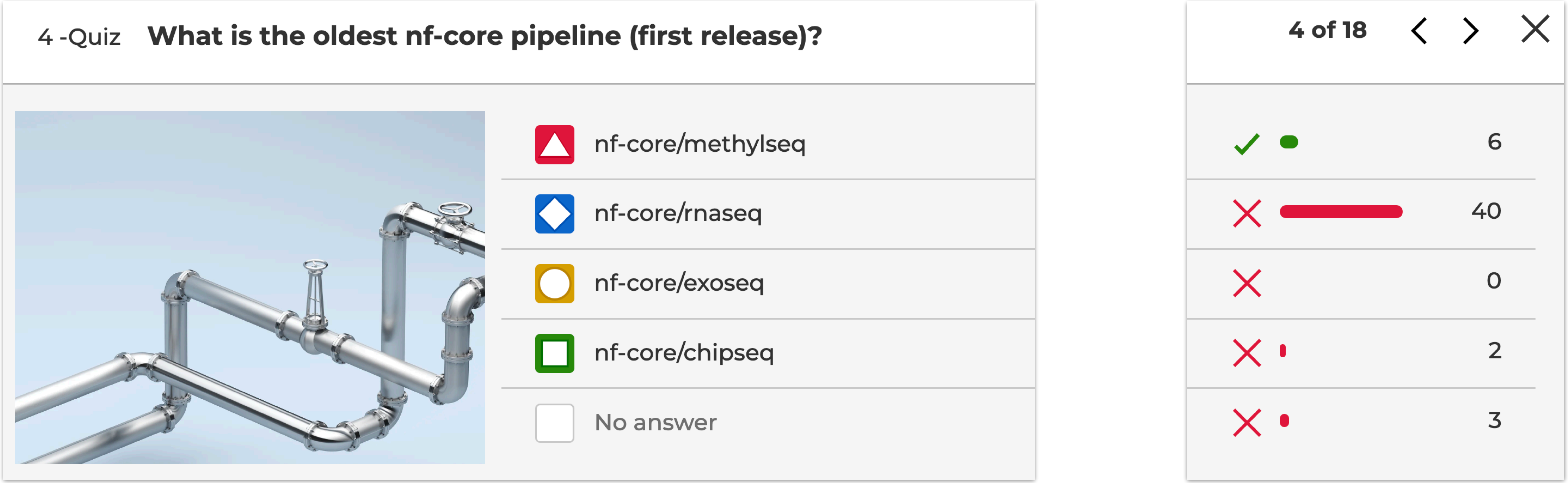
6 -Quiz **How many bytesize talks are currently there? (2022-10-10)**

6 of 18

▲	51	✓	6
◆	42	✗	21
●	53	✗	7
■	46	✗	14
☐	No answer	✗	3

Kahoot


12%


4 -Quiz **What is the oldest nf-core pipeline (first release)?**

4 of 18

▲	nf-core/methylseq	✓	6
◆	nf-core/rnaseq	✗	40
●	nf-core/exoseq	✗	0
■	nf-core/chipseq	✗	2
☐	No answer	✗	3

Kahoot

82%

11 -Quiz **What type of apple is most likely the nf-core logo one?**

1 of 18

▲	Golden Delicious	✗	4
◆	Honeycrisp	✗	0
●	Pink Lady	✗	1
■	Granny smith	✓	42
☐	No answer	✗	4

Kahoot

Maxime

2

11486

12 out of 18

Mashehu

1

11541

12 out of 18

Nicolas V

3

11120

12 out of 18

Community

Community

https://nf-co.re

Thank you!

nf-core/
hackathon

October
2022